

T7 primer
TTAATACGACTCACTATAGGG AGACCGG AAG CTT AAG GTG CAC GGC CCA CGT GGA TCG ATC GCG CGC AGA TCT TCG GAA
Hind 3 Bgl II

-28

Met	Asp	Ser	Lys	Val	Thr	Ile	Ile	Cys	Ile	Arg	Phe	Leu	Phe	Trp	Phe	Leu	Leu	Leu	Cys	Met	Leu	Ile	Gly	Lys	Ser	His	Thr		
GCC	ACC	ATG	GAT	AGC	AAA	GTC	ACA	ATC	ATA	TGC	ATC	AGA	TTT	CTC	TTT	TGG	TTT	CTT	TG	CTC	TGC	ATG	CTT	ATT	GGG	AAG	TCA	CAT	ACT
+1	NcoI															CHO													
Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly
GAA	GAT	GAC	ATC	ATA	ATT	GCA	ACA	AAG	AAT	GGA	AAA	GTC	AGA	GGG	ATG	AAC	TTG	ACA	GTT	TTT	GGT	GGC	ACG	GTA	ACA	GCC	TTT	CTT	GGA
																													90
Ile	Pro	Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys
ATT	CCC	TAT	GCA	CAG	CCA	CCT	CTT	GCT	AGA	CTT	CGA	TTC	AAA	AAG	CCA	CAG	TCT	CTG	ACC	AAG	TGG	TCT	GAT	ATT	TGG	AAT	GCC	ACA	AAA
Eco RI																													180
Tyr	Ala	Asn	Ser	Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu
TAT	GCA	AAT	TCT	TGC	TGT	CAG	AAC	ATA	GAT	CAA	AGT	TTT	CCA	GGC	TTC	CAT	GGA	TCA	GAG	ATG	TGG	AAC	CCA	AAC	ACT	GAC	CTC	AGT	GAA
																													270
Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr
GAC	TGT	TTA	TAT	CTA	AAT	GTA	TGG	ATT	CCA	GCA	CCT	AAA	CCA	AAA	AAT	GCC	ACT	GTA	TTG	ATA	TGG	ATT	TAT	GGT	GGT	GGT	TTT	CAA	ACT
																													360
Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr	Arg	Val	Gly	Ala
GGA	ACA	TCA	TCT	TTA	CAT	GTT	TAT	GAT	GGC	AAG	TTT	CTG	GCT	CGG	GTT	GAA	AGA	GTT	ATT	GTA	GTG	TCA	ATG	AAC	TAT	AGG	GTG	GGT	GCC
																													450
Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	Val	Gln	Lys
CTA	GGA	TTC	TTA	GCT	TTG	CCA	GGA	AAT	CCT	GAG	GCT	CCA	GGG	AAC	ATG	GGT	TTA	TTT	GAT	CAA	CAG	TTG	GCT	CTT	CAG	TGG	GTT	CAA	AAA
																													540
Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	Leu	Phe	Gly	Glu	SER	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	Ser
AAT	ATA	GCA	GCC	TTT	GGT	GGA	AAT	CCT	AAA	AGT	GTA	ACT	CTC	TTT	GGA	GAA	AGT	GCA	GGA	GCA	GCT	TCA	GTT	AGC	CTG	CAT	TTG	CTT	TCT
																													630
Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
CCT	GGA	AGC	CAT	TCA	TTG	TTC	ACC	AGA	GCC	ATT	CTG	CAA	AGT	GGT	TCC	TTT	AAT	GCT	CCT	TGG	GCG	GTA	ACA	TCT	CTT	TAT	GAA	GCT	AGG
CHO																													720
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln
AAC	AGA	ACG	TTG	AAC	TTA	GCT	AAA	TTG	ACT	GGT	TGC	TCT	AGA	GAG	AAT	GAG	ACT	GAA	ATA	ATC	AAG	TGT	CTT	AGA	AAT	AAA	GAT	CCC	CAA
																													810
Glu	Ile	Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr
GAA	ATT	CTT	CTG	AAT	GAA	GCA	TTT	GTT	GTC	CCC	TAT	GGG	ACT	CCT	TTG	TCA	GTA	AAC	TTT	GGT	CCG	ACC	GTG	GAT	GGT	GAT	TTT	CTC	ACT
																													900
Asp	Met	Pro	Asp	Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	Asn	Lys	Asp	Glu	Gly	Thr	Trp	Phe	Leu
GAC	ATG	CCA	GAC	ATA	TTA	CTT	GAA	CTT	GGA	CAA	TTT	AAA	AAA	ACC	CAG	ATT	TTG	GTG	GGT	GTT	AAT	AAA	GAT	GAA	GGG	ACA	TGG	TTT	TTA
																													990
Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly
GTC	TAT	GGT	GCT	CCT	GGC	TTC	AGC	AAA	GAT	AAC	AAT	AGT	ATC	ATA	ACT	AGA	AAA	GAA	TTT	CAG	GAA	GGT	TTA	AAA	ATA	TTT	TTT	CCA	GGA
																													1080
Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	Tyr	Arg	Glu	Ala	Leu	Gly
GTG	AGT	GAG	TTT	GGA	AAG	GAA	TCC	ATC	CTT	TTT	CAT	TAC	ACA	GAC	TGG	GTA	GAT	GAT	CAG	AGA	CCT	GAA	AAC	TAC	CGT	GAG	GCC	TTG	GGT
																													1170
Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	Phe	Phe	Tyr	Tyr
GAT	GTT	GTT	GGG	GAT	TAT	AAT	TTC	ATA	TGC	CCT	GCC	TTG	GAG	TTC	ACC	AAG	AAG	TTC	TCA	GAA	TGG	GGA	AAT	AAT	GCC	TTT	TTC	TAC	TAT
																													1260
Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	Pro	Leu
TTT	GAA	CAC	CGA	TCC	TCC	AAA	CTT	CCG	TGG	CCA	GAA	TGG	ATG	GGA	GTG	ATG	CAT	GGC	TAT	GAA	ATT	GAA	TTT	GTC	TTT	GGT	TTA	CCT	CTG
																													1350
Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
GAA	AGA	AGA	GAT	AAT	TAC	ACA	AAA	GCC	GAG	GAA	ATT	TTG	AGT	AGA	TCC	ATA	GTG	AAA	CGG	TGG	GCA	AAT	TTT	GCA	AAA	TAT	GGG	AAT	CCA
																													1440
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile
AAT	GAG	ACT	CAG	AAC	AAT	AGC	ACA	AGC	TGG	CCT	GTC	TTC	AAA	AGC	ACT	GAA	CAA	AAA	TAT	CTA	ACC	TTG	AAT	ACA	GAG	TCA	ACA	AGA	ATA
																													1530
Met	Thr	Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu
ATG	ACG	AAA	CTA	CGT	GCT	CAA	CAA	TGT	CGA	TTC	TGG	ACA	TCA	TTT	TTT	CCA	AAA	GTC	TTG	GAA	ATG	ACA	GGA	AAT	ATT	GAT	GAA	GCA	GAA
																													1620

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EDDIIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTK
WSDIWNATKYANSCCONIDOSFPGFHGSEMWNPNNTDLSCLYLNWVWIPAP
KPKNATVLIWIIYGGGFOTGTSSLHVYDYGKFLARVERVIVVSMNYRVGALGF
LALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASV
SLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRE
NETEIIKCLRNKDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLTDMPDIL
LELGQFKKTQILVGVNKDEGTAEFLVYGAPGFSKDNNSSIITRKEFQEGLKIF
FPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDDYNFICPALEFTKK
FSEWGNNAFFYYFEHRSSKLPWPPEWMGVMHGYEIEFVFGGLPLERRDNYTKA
EEILSR SIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLTNTTESTRI
MTKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQF
NDYTSKKESCVGL

FIGURE 2

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1  tactgaatgt cagtgcagtc caatttacag gctggagcag cagctgcata ctgcatttcc
61 ccgaagtatt acatgatatt cactccttgc aaactttacc atctttgttg cagagaatcg
121 gaaatcaata tgcatagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt
181 ttgctctgca tgcattattg gaagtcacat actgaagatg acatcataat tgcaacaaag
241 aatggaaaag tcagagggat gaacttgaca gtttttgggt gcacggtaac agcctttctt
301 ggaattccct atgcacagcc acctcttggt agacttcgal tcaaaaagcc acagtctctg
361 accaagtggg ctgatatttg gaatgccaca aaatatgcaa attcttgctg tcagaacata
421 gatcaaagtt ttccaggctt ccatggatca gagatgtgga acccaaacac tgacctcagt
481 gaagactggt tatatctaaa tgtatggatt ccagcaccta aacccaaaaa tgccactgta
541 ttgatattga tttatgggtg tggttttcaa actggaacat catctttaca tgtttatgat
601 ggcaagtttc tggctcgggt tgaaagagtt attgtagtgt caatgaacta taggggtgggt
661 gccctaggat tcttagcttt gccaggaaat cctgaggctc cagggaacat ggggtttattt
721 gatcaacagt tggctcttca gtgggttcaa aaaaatatag cagcctttgg tggaaatcct
781 aaaagtgtaa ctctctttgg agaaagtgca ggagcagctt cagttagcct gcatttgctt
841 tctcctggaa gccattcatt gtaccacaga gccattctgc aaagtggatc ctttaatgct
901 ccttggggcg taacatctct ttatgaagct aggaacagaa cgttgaactt agctaaattg
961 actggttgct ctagagagaa tgagactgaa ataatcaagt gtcttagaaa taaagatccc
1021 caagaaattc ttctgaatga agcatttggt gtccctatg ggactccttt gtcagtaaac
1081 tttgggtccg ccgtggatgg tgattttctc actgacatgc cagacatatt acttgaactt
1141 ggacaattta aaaaaacca gattttgggt ggtgttaata aagatgaagg gacagctttt
1201 ttagtctatg gtgctcctgg cttcagcaaa gataacaata gtatcataac tagaaaagaa
1261 tttcaggaag gtttaaaaat attttttcca ggagtgagtg agtttggaag ggaatccatc
1321 ctttttcatt acacagactg ggtagatgat cagagacctg aaaactaccg tgaggccttg
1381 ggtgatgttg ttggggatta taatttcata tgccctgcct tggagttcac caagaagttc
1441 tcagaatggg gaaataatgc ctttttctac tattttgaac accgatcctc caaacttccg
1501 tggccagaat ggatgggagt gatgcatggc tatgaaattg aatttgtctt tggtttacct
1561 ctggaaagaa gagataatta cacaaaagcc gaggaatttt tgagtagatc catagtgaag
1621 cgggtgggcaa attttgcaaa atatgggaat ccaaatgaga ctcagaacaa tagcacaagc
1681 tggcctgtct tcaaaaagcag tgaacaaaaa tatctaacct tgaatacaga gtaacaaga
1741 ataatgacga aactacgtgc tcaacaatgt cgattctgga catcattttt tccaaaagtc
1801 ttggaaatga caggaaatat tgatgaagca gaatgggagt ggaaagcagg attccatcgc
1861 tggaacaatt acatgatgga ctggaaaaat caatttaacg attacactag caagaaagaa
1921 agttgtgtgg gtctctaatt aatagattta ccctttatag aacatatitt cctttagatc
1981 aaggcaaaaa tatcaggagc ttttttacac acctactaaa aaagttatta tgtagctgaa
2041 acaaaaatgc cagaaggata atattgatgc ctcacatctt taacttagta ttttacctag
2101 catttcaaaa cccaaatggc tagaacatgt ttaattaaat ttcacaatat aaagttctac
2161 agttaattat gtgcatatta aaacaatggc ctggttcaat ttctttcttt ccttaataaa
2221 ttttaagttt ttccccccaa aattatcagt gctctgcttt tagtcacgtg tattttcatt
2281 accactcgta aaaaggtatc ttttttaaat gaattaaata ttgaaacact gtacaccata
2341 gtttacaata ttatgtttcc taattaaaat aagaattgaa tgtcaatatg agatattaaa
2401 ataagcacag aaaatc

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Figure 3. Nucleic acid sequence of human butyrylcholinesterase (SEQ ID NO: 16)
Genbank accession number M16541.

FIGURE 3

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human wild-type BChE	1	10	20	30
human A variant BChE	EDDIIIATKN	GKVRGMNLTV	FGGTVTAFLG	
human J variant BChE	-----	-----	-----	
human K variant BChE	-----	-----	-----	
rat BChE	EEDVIITTKT	GRVRGLSMPI	LG GTVTAFLG	
cat BChE	EEDIIITTKN	GKVRGMNLPV	LD GTVTAFLG	
horse BChE	EEDIIITTKN	GKVRGMNLPV	LG GTVTAFLG	

	40	50	60	70	80	90	100
human wt	IPYAQPPLGR	LRFKKPQSLT	KWSDIWNATK	YANSCCQNID	QSFPGFHGSE	MWNPNTDLSE	DCLYLN VWIP
human A	-----	-----	-----	-----G	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	IPYAQPPLGS	LRFKKPQPLN	KWPDVYNATK	YANSCYQNID	QAFPGFQGSE	MWNPNTNLSE	DCLYLN VWIP
cat	IPYAQPPLGR	LRFKKPQFLT	KWSDIWNATK	YANSCYQNAD	QSFPGFPGSE	MWNPNTDLSE	DCLYLN VWIP
horse	IPYAQPPLGR	LRFKKPQSLT	KWSNIWNATK	YANSCYQNTD	QSFPGFGLSE	MWNPNTLSE	DCLYLN VWIP

	110	120	130	140	150	160	170
human wt	APKPKNATVL	IWIYGGGFQT	GTSSLHVDYG	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EAPGNMGLFD
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	VPKPKNATVM	VWVYGGGFQT	GTSSLPVYDG	KFLTRVERVI	VVSMNYRVGA	LGFLAFPGNS	EAPGNMGLFD
cat	TPKPKNATVM	IWIYGGGFQT	GTSSLPVYDG	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EVPGNMGLFD
horse	APKPKNATVM	IWIYGGGFQT	GTSSLPVYDG	KFLARVERVI	VVSMNYRVGA	LGFLALSEN	EAPGNMGLFD

	180	190	200	210	220	230	240
human wt	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AASVSLHLLS	PGSHSLFTRA	ILQSGSFNAP	WAVTSLYEAR
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AASVSLHLLC	PQSYPLFTRA	ILES GSSNAP	WAVKHPEEAR
cat	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AGSVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVMSLDEAK
horse	QQLALQWVQK	NIAAFGGNPR	SVTLFGESAG	AASVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVTSLYEAR

	250	260	270	280	290	300	310
human wt	NRTLNLAKLT	GCSRENETEI	IKCLRNDKPQ	EILLNEAFVV	PYGTPLSVNF	GPTVDGDFLT	DMPDILLELG
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	NRTLTLAKFI	GCSKENEKEI	ITCLRSKDPQ	EILLNEKLVL	PSDSIRSINF	GPTVDGDFLT	DMPHTLLQLG
cat	NRTLTLAKFI	GCSKENDTEI	IKCLRNDKPQ	EILLNELLVV	PSDTLLSVNF	GPVVDGDFLT	DMPDTLLQLG
horse	NRTLTLAKRM	GCSRDNETEM	IKCLRNDKPQ	EILLNEVFVV	PYDTLLSVNF	GPTVDGDFLT	DMPDTLLQLG

	320	330	340	350	360	370	380
human wt	QFKKTQILVG	VNKDEGTAFL	YVGAPGFSKD	NNSIITRKEF	QEGLKIFFPG	VSEFGKESIL	FHYTDWVDDQ
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	KVKTAQILVG	VNKDEGTAFL	YVGAPGFSKD	NDSLITRREF	QEGLNMYFPG	VSSLGKEAIL	FYYVDWLGDQ
cat	QFKKTQILVG	VNKDEGTAFL	YVGAPGFSKD	NDSIITRKEF	QEGLKIYFPG	VSEFGREAIL	FYYVDLLDDQ
horse	QFKRTQILVG	VNKDEGTAFL	YVGAPGFSKD	NNSIITRKEF	QEGLKIFFPR	VSEFGRESIL	FHYMDWLDDQ

FIGURE 4 (PAGE 1 OF 2)

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	390	400	410	420	430	440	450
human wt	RPENYREALG	DVVGDDYNFIC	PALEFTKKFS	EWGNNAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFGGLPL
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	TPEVYREAFD	DIIGDYNIC	PALEFTKKFA	ELEINAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFGGLPL
cat	RAEKYREALD	DVLGDYNIIC	PALEFTTKFS	ELGNNAFFYY	FEHRSSQLPW	PEWMGVMHGY	EIEFVFGGLPL
horse	RAENYREALD	DVVGDDYNIIC	PALEFTRKFS	ELGNDAFFYY	FEHRSTKLPW	PEWMGVMHGY	EIEFVFGGLPL

	460	470	480	490	500	510	520
human wt	ERRDNYTKAE	EILSRIVKR	WANFAKYGNP	NETQNNSTSW	PVFKSTEQKY	LTLNTESTRI	MTKLRAQQCR
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----V-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	ERRVNYTRAE	EIFSRSIMKT	WANFAKYGHP	NGTQGNSTVW	PVFTSTEQKY	LTLNTEKSKI	NSKLRAQQCQ
cat	ERRVNYTRAE	EILSRSIMNY	WANFAKYGNP	NGTQNNSTRW	PAFRSTDQKY	LTLNABSPKV	YTKLRAQQCR
horse	ERRVNYTRAE	EILSRSIMKR	WANFAKYGNP	NGTQNNSTRW	PVFKSTEQKY	LTLNTESPKV	YTKLRAQQCR

	530	540	550	560	570	574
human wt	FWTSFFPKVL	EMTGNIIDEAE	WEWKAGFHRW	NNYMMDWKNQ	FNDYTSKKES	CVGL
human A	-----	-----	-----	-----	-----	---
human J	-----	-----	-----	-----	-----	---
human K	-----	-----T-----	-----	-----	-----	---
rat	FWRLFFPKVL	EITGDIDERE	QEWKAGFHRW	SNYMMDWKNQ	FNDYTSKKET	CTDL
cat	FWTLFFPKVL	EMTGNIIDEAE	REWRAGFYRW	NNYMMDWKNQ	FNDYTSKKES	CAGL
horse	FWTLFFPKVL	ELTGNIIDEAE	REWKAGFHRW	NNYMMDWKNQ	FNDYTSKKES	CSDF

FIGURE 4 (PAGE 2 OF 2)

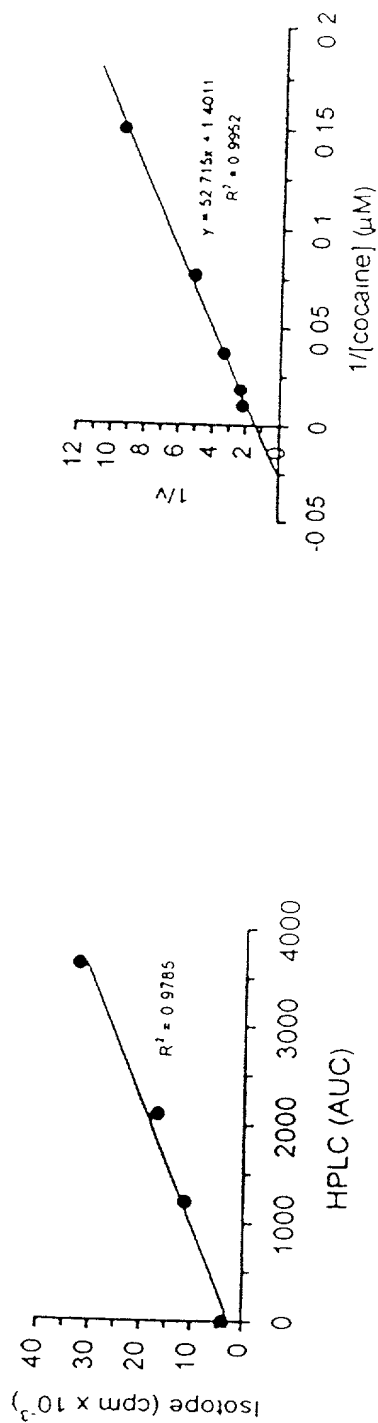


FIGURE 5

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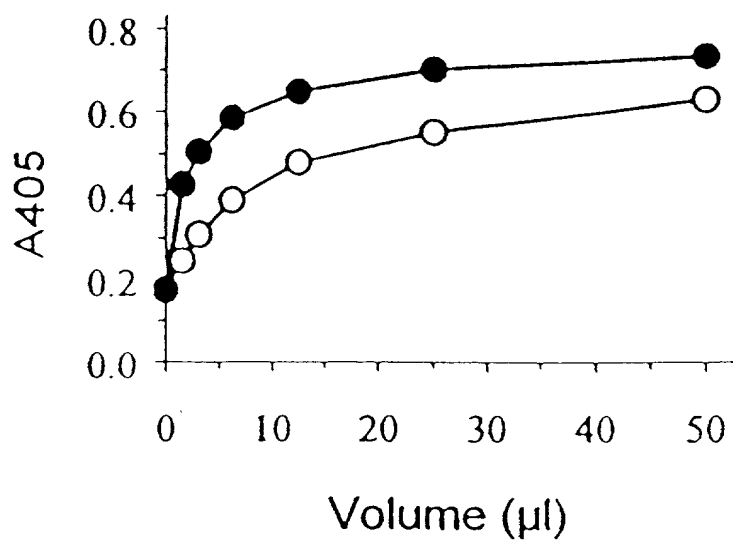


FIGURE 6

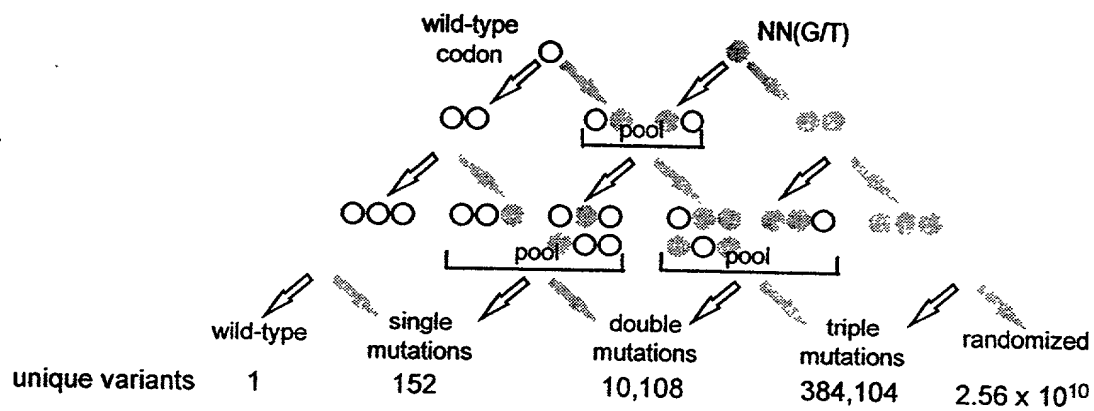


FIGURE 7